

# SEQUENCE LISTING

<110> TEPPER, Mark  
CUNNINGHAM, Mark  
SHERRIS, David  
EL TAYAR, Nabil  
McKENNA, Sean

<120> IFNAR2/IFN COMPLEX

<130> TEPPER1A.SEQ

<140> not yet received

<141> 1998-12-18

<150> 60/068,295

<151> 1997-12-19

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 5

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 1

Gly Gly Gly Gly Ser

1

5

<210> 2

<211> 4

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 2

Ile Glu Glu Arg

1

<210> 3  
<211> 33  
<212> PRT  
<213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 3

Glu Ser Glu Phe Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Met Ser  
20 25 30

Tyr

<210> 4  
<211> 28  
<212> PRT  
<213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 4

Glu Ser Glu Phe Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Met Ser Tyr  
20 25

<210> 5  
<211> 23  
<212> PRT  
<213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 5

Glu Ser Glu Phe Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

Gly Gly Gly Ser Met Ser Tyr

<210> 6  
 <211> 18  
 <212> PRT  
 <213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 6

Glu Ser Glu Phe Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Met  
 1 5 10 15

Ser Tyr

<210> 7  
 <211> 13  
 <212> PRT  
 <213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 7

Glu Ser Glu Phe Ser Gly Gly Gly Gly Ser Met Ser Tyr  
 1 5 10

<210> 8  
 <211> 36  
 <212> PRT  
 <213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 8

Glu Ser Glu Phe Ser Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu  
 1 5 10 15

Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro  
 20 25 30

Gln Met Ser Tyr

<210> 9  
 <211> 23  
 <212> PRT  
 <213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 9

Glu Ser Glu Phe Ser Glu Phe Met Glu Phe Met Glu Phe Met Glu Phe  
 1 5 10 15

Met Glu Phe Met Met Ser Tyr  
 20

<210> 10  
 <211> 20  
 <212> PRT  
 <213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 10

Glu Ser Glu Phe Ser Glu Phe Met Glu Phe Met Glu Phe Met Glu Phe  
 1 5 10 15

Met Met Ser Tyr  
 20

<210> 11  
 <211> 17  
 <212> PRT  
 <213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 11

Glu Ser Glu Phe Ser Glu Phe Met Glu Phe Met Glu Phe Met Met Ser  
 1 5 10 15

Tyr

<210> 12  
<211> 21  
<212> PRT  
<213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 12

Glu Ser Glu Phe Ser Glu Phe Gly Ala Gly Leu Val Leu Gly Gly Gln  
1 5 10 15

Phe Met Met Ser Tyr  
20

<210> 13  
<211> 34  
<212> PRT  
<213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 13

Glu Ser Glu Phe Ser Glu Phe Gly Ala Gly Leu Val Leu Gly Gly Gln  
1 5 10 15

Phe Met Glu Phe Gly Ala Gly Leu Val Leu Gly Gly Gln Phe Met Met  
20 25 30

Ser Tyr

<210> 14  
<211> 400  
<212> PRT  
<213> Unknown

<220>

<223> Description of Unknown Organism: Peptide

<400> 14

Met Leu Leu Ser Gln Asn Ala Phe Ile Val Arg Ser Leu Asn Leu Val

1                      5                      10                      15  
 Leu Met Val Tyr Ile Ser Leu Val Phe Gly Ile Ser Tyr Asp Ser Pro  
                     20                      25                      30  
 Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys Ile Ser Leu Arg Asn Phe  
                     35                      40                      45  
 Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn His Ser Ile Val Pro Thr  
                     50                      55                      60  
 His Tyr Thr Leu Leu Tyr Thr Ile Met Ser Lys Pro Glu Asp Leu Lys  
                     65                      70                      75                      80  
 Val Val Lys Asn Cys Ala Asn Thr Thr Arg Ser Phe Cys Asp Leu Thr  
                     85                      90                      95  
 Asp Glu Trp Arg Ser Thr His Glu Ala Tyr Val Thr Val Leu Glu Gly  
                     100                      105                      110  
 Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys Ser His Asn Phe Trp Leu  
                     115                      120                      125  
 Ala Ile Asp Met Ser Phe Glu Pro Pro Glu Phe Glu Ile Val Gly Phe  
                     130                      135                      140  
 Thr Asn His Ile Asn Val Met Val Lys Phe Pro Ser Ile Val Glu Glu  
                     145                      150                      155                      160  
 Glu Leu Gln Phe Asp Leu Ser Leu Val Ile Glu Glu Gln Ser Glu Gly  
                     165                      170                      175  
 Ile Val Lys Lys His Lys Pro Glu Ile Lys Gly Asn Met Ser Gly Asn  
                     180                      185                      190  
 Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro Asn Thr Asn Tyr Cys Val  
                     195                      200                      205  
 Ser Val Tyr Leu Glu His Ser Asp Glu Gln Ala Val Ile Lys Ser Pro  
                     210                      215                      220  
 Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln Glu Ser Glu Phe Ser Gly  
                     225                      230                      235                      240  
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Met Ser Tyr Asn Leu Leu Gly  
                     245                      250                      255  
 Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln

260

265

270

Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp  
 275 280 285

Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala  
 290 295 300

Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg  
 305 310 315 320

Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu  
 325 330 335

Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu  
 340 345 350

Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser  
 355 360 365

Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala  
 370 375 380

Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu  
 385 390 395 400